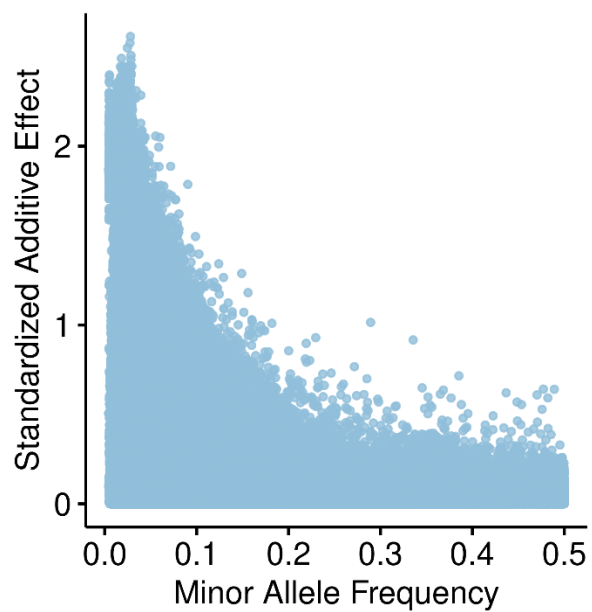
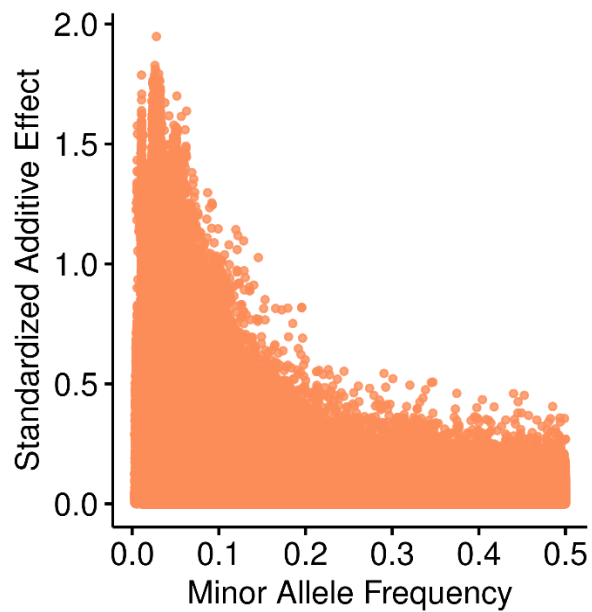


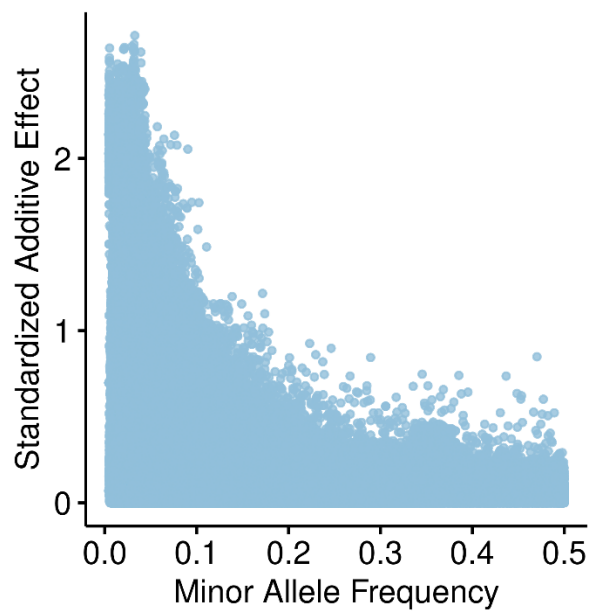
Teosinte: DTA



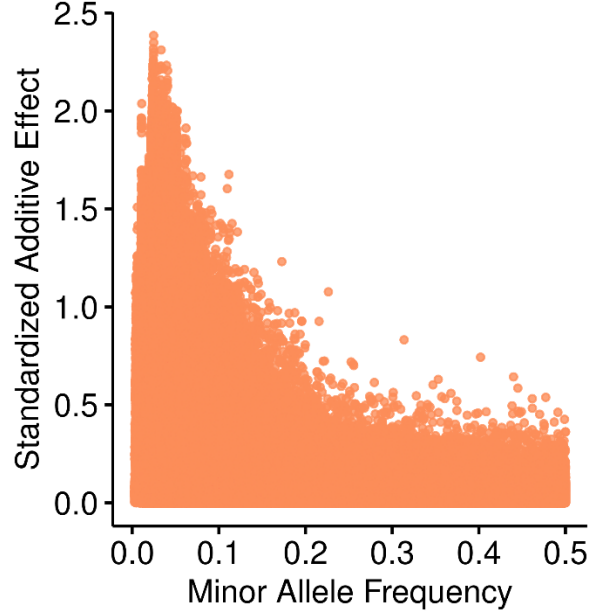
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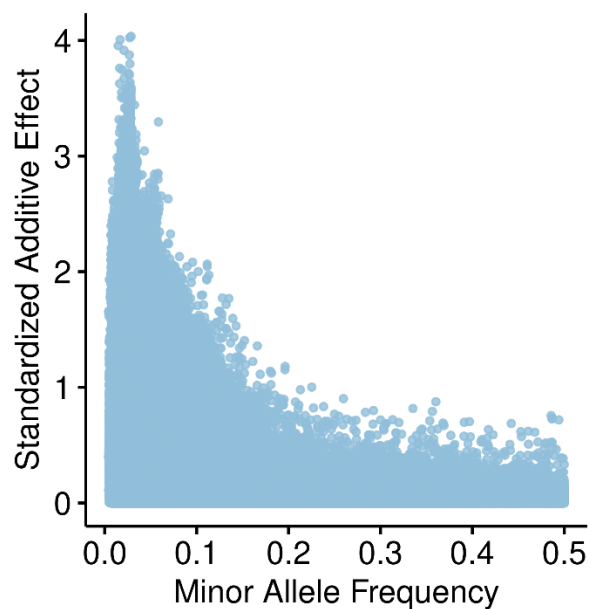
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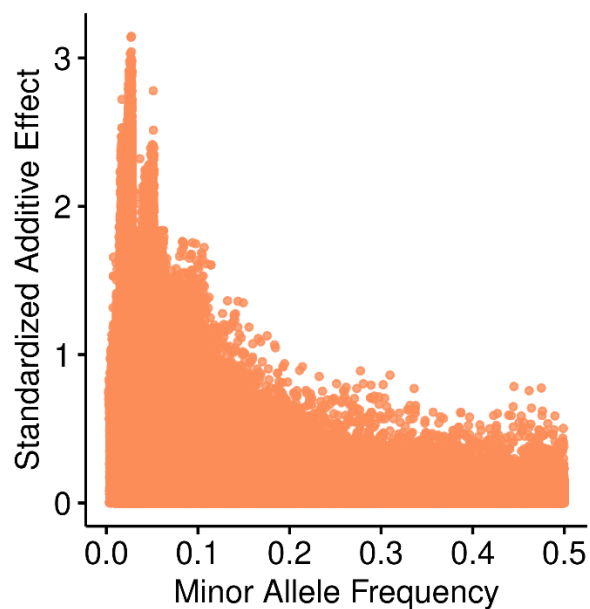
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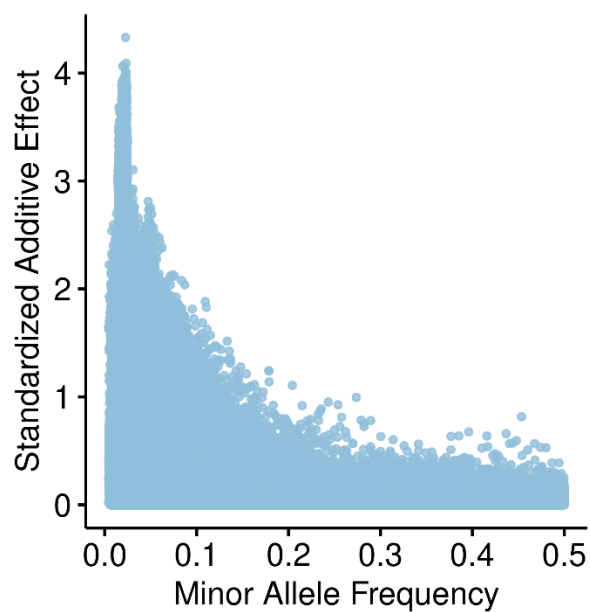
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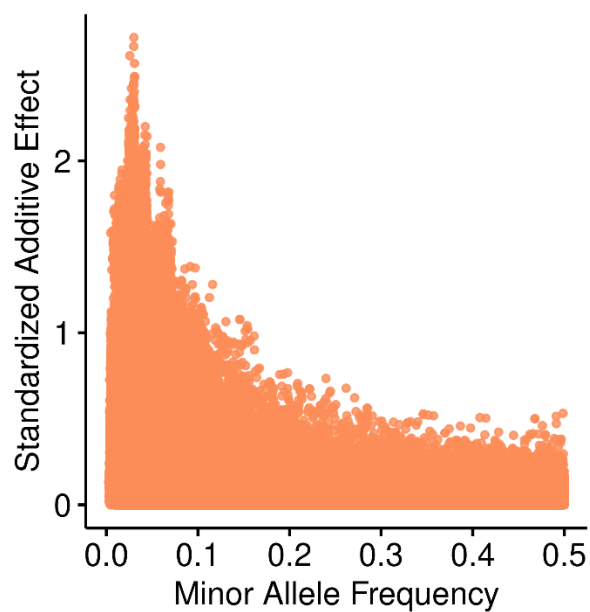
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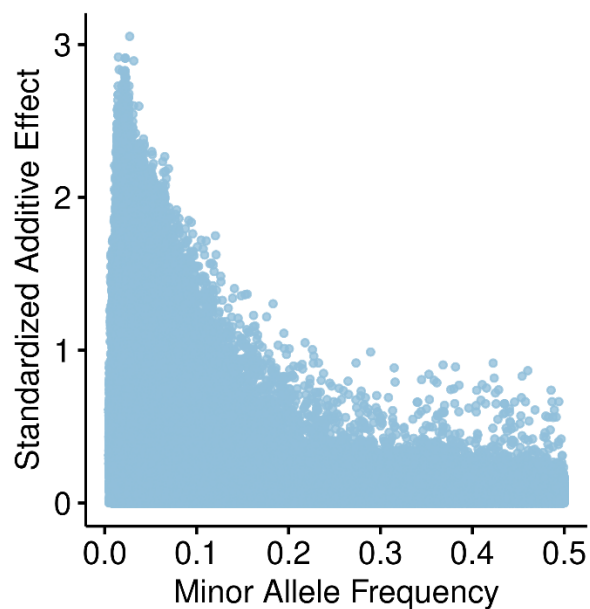
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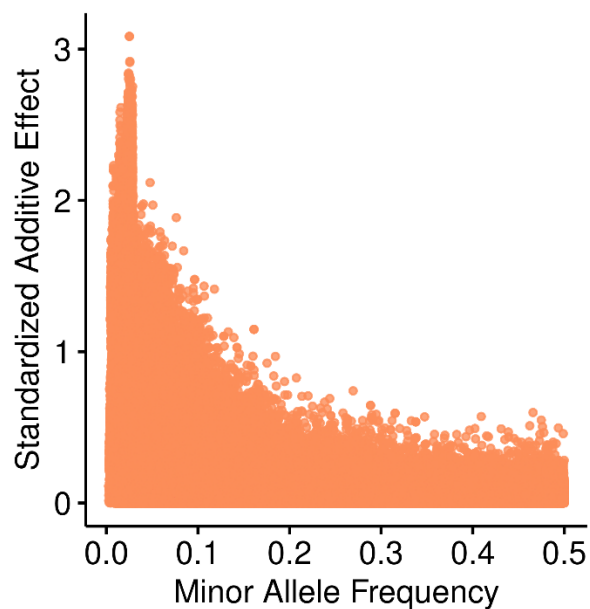
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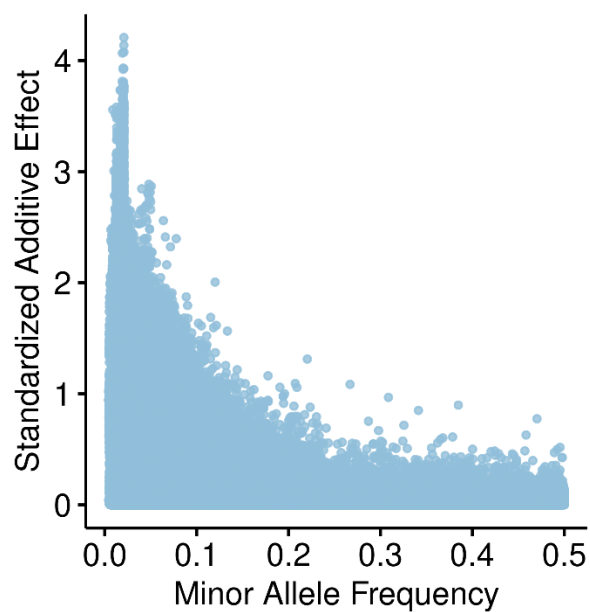
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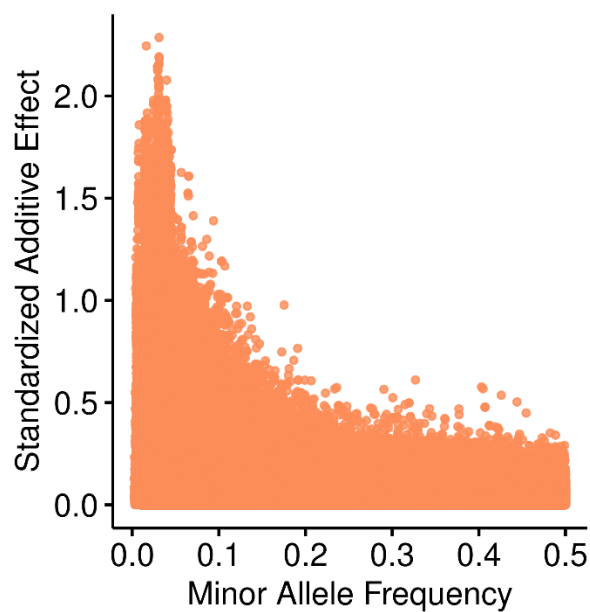
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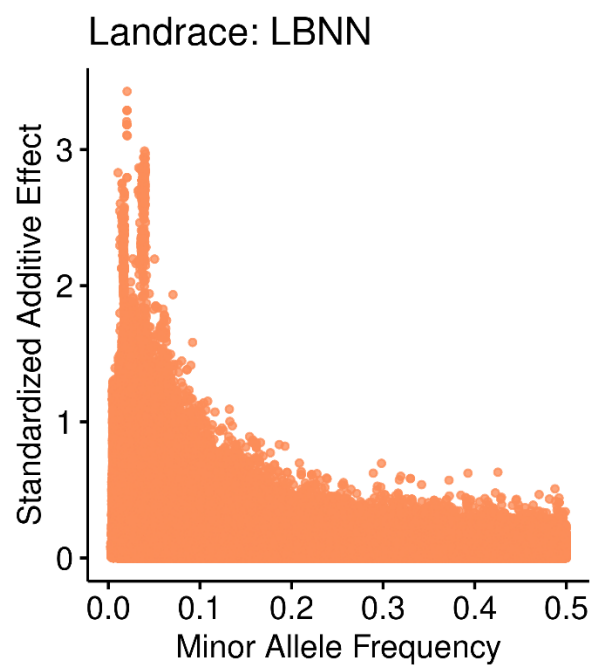
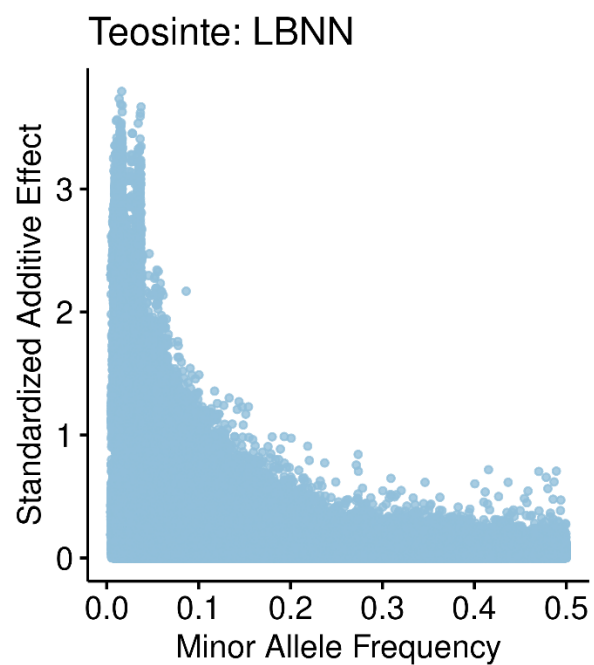
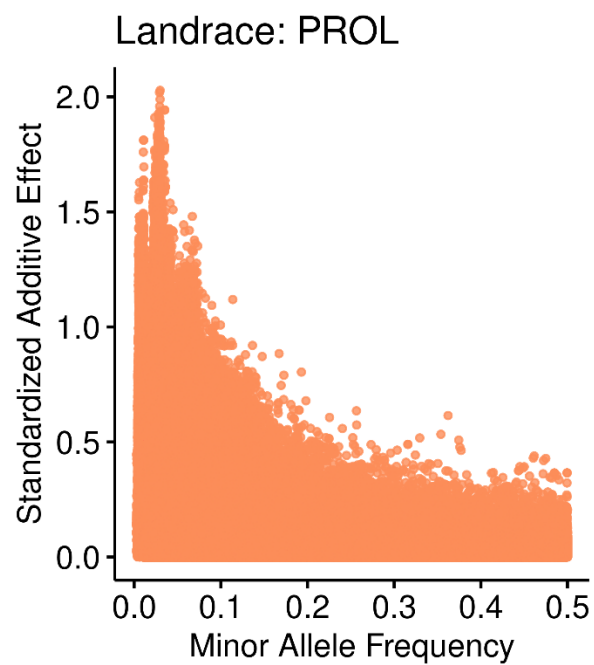
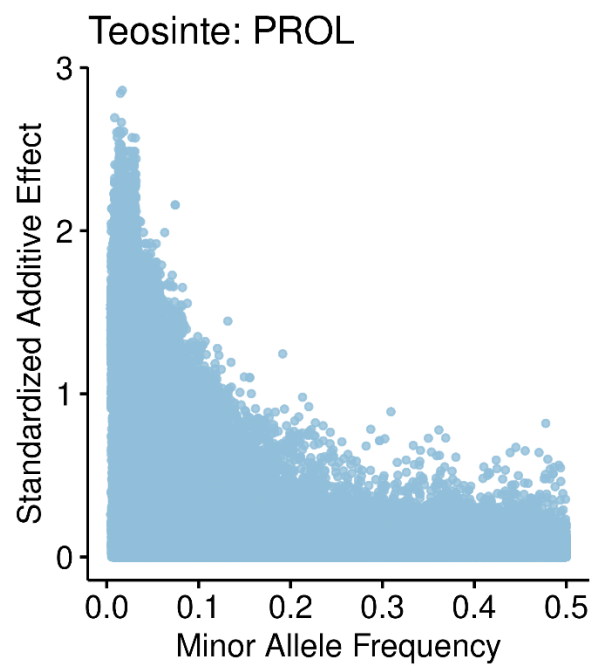


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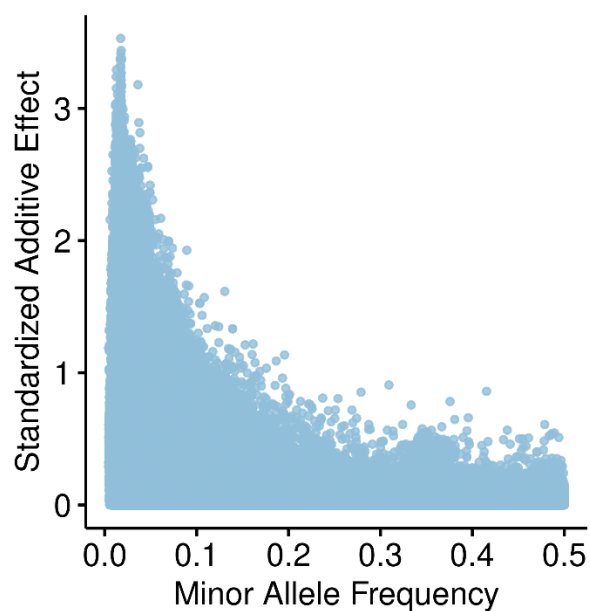


Landrace: TILN

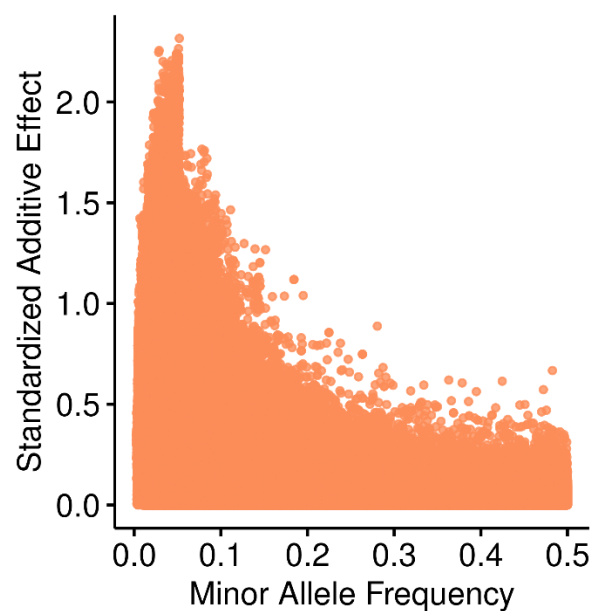




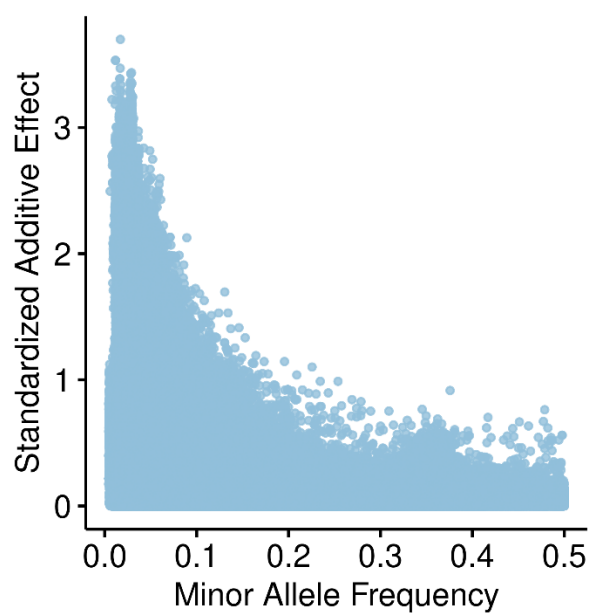
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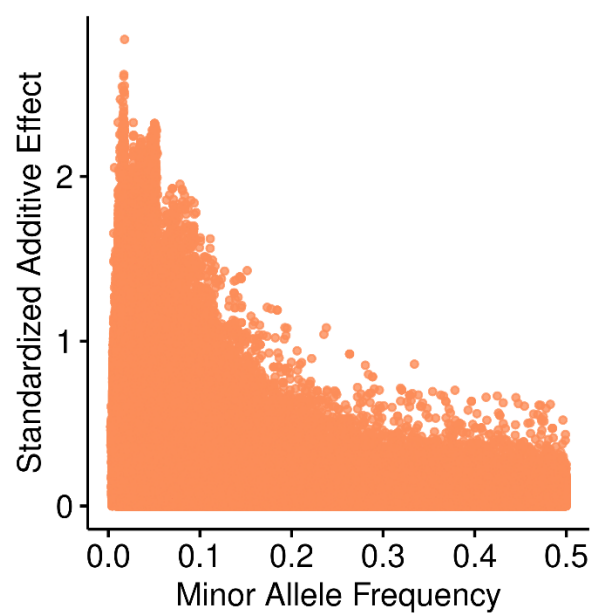
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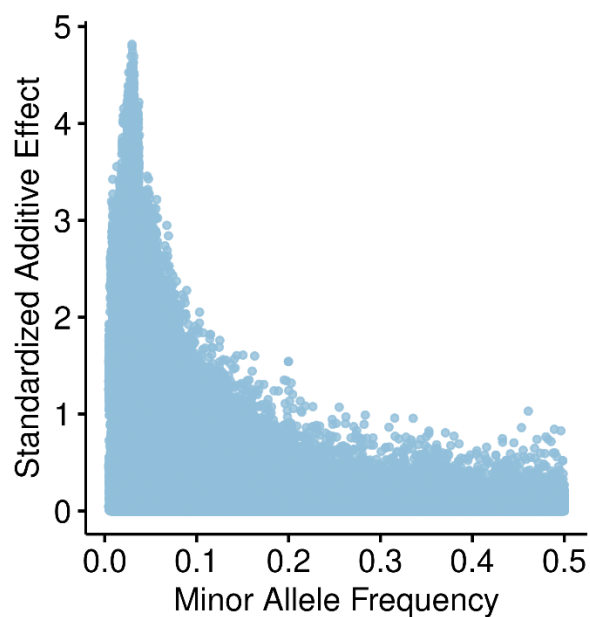
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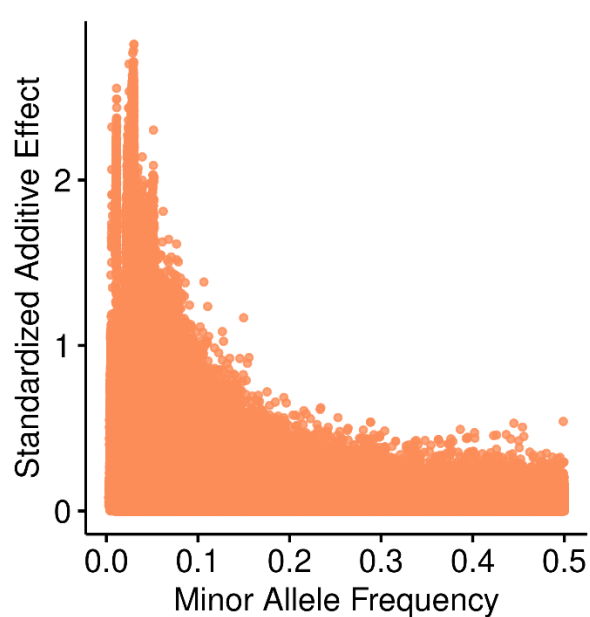
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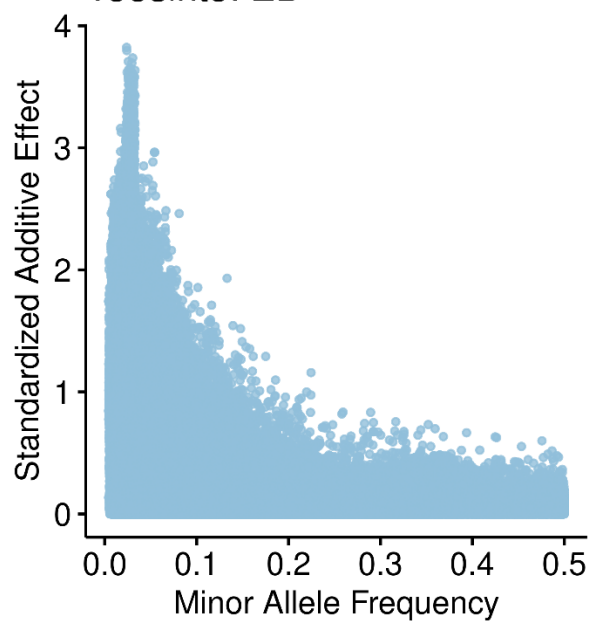
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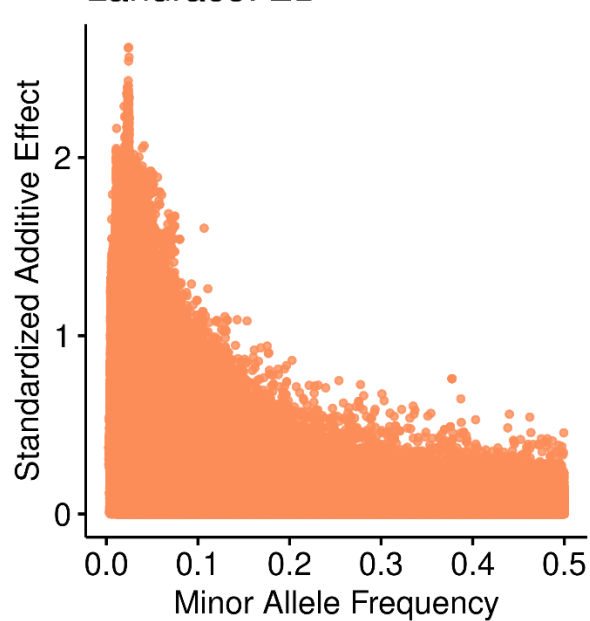
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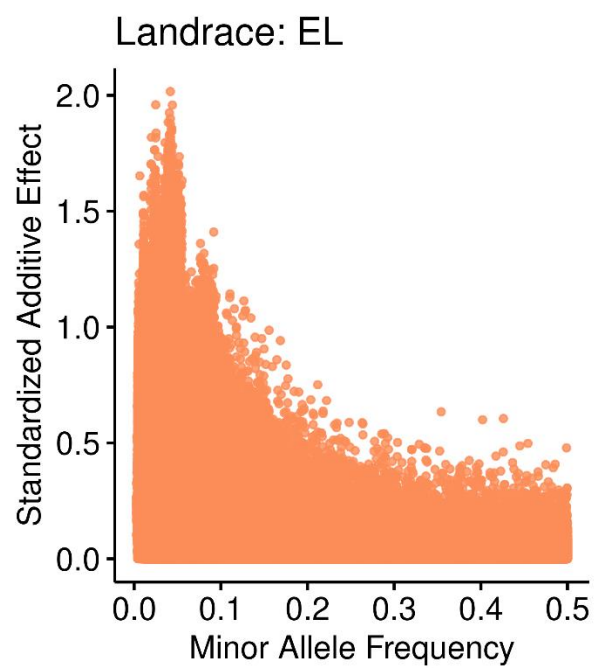
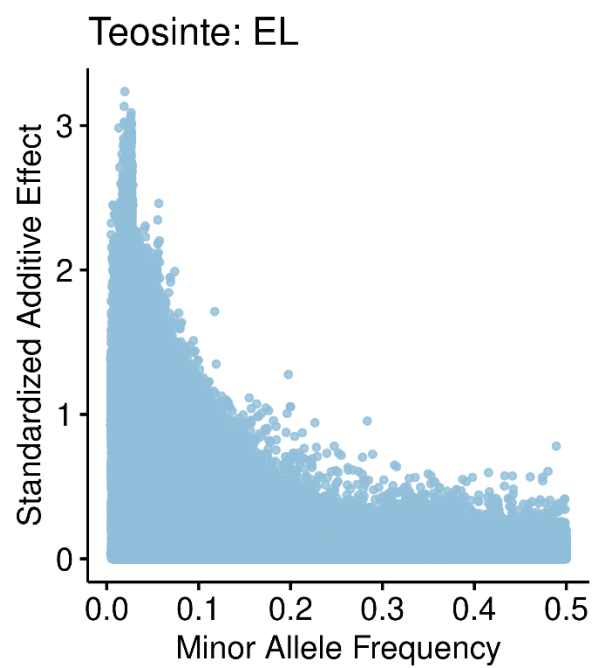
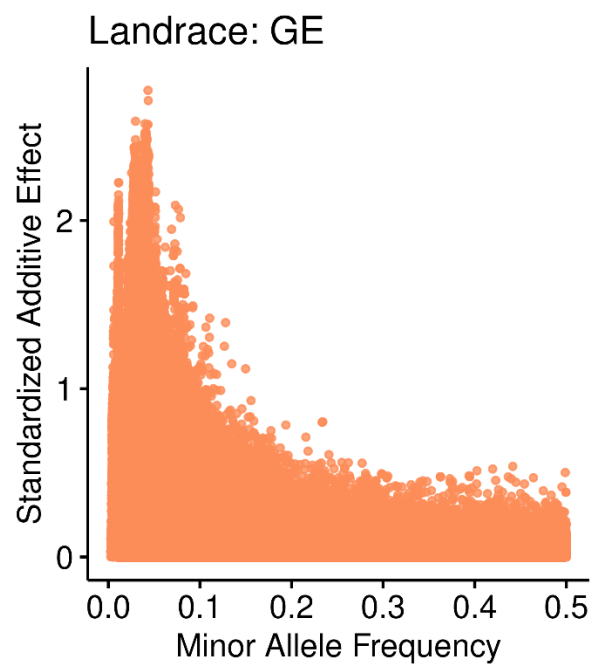
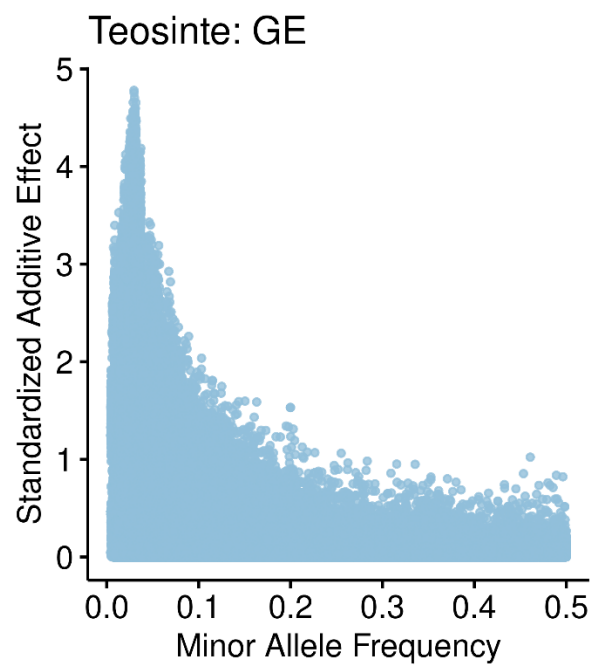


Teosinte: ED

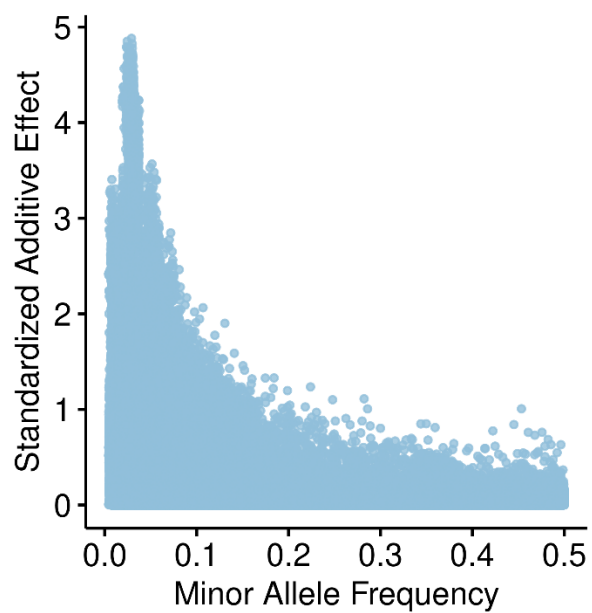


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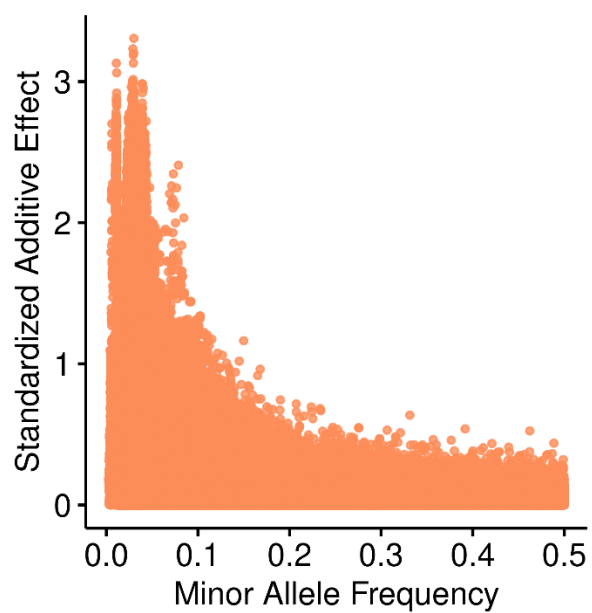




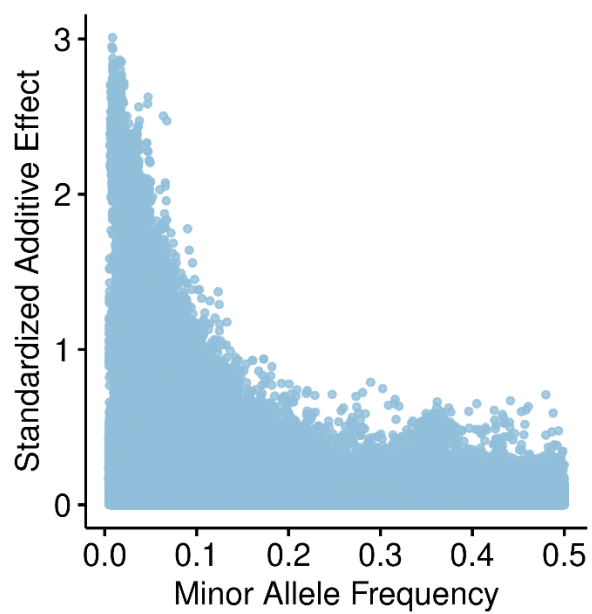
Teosinte: EILN



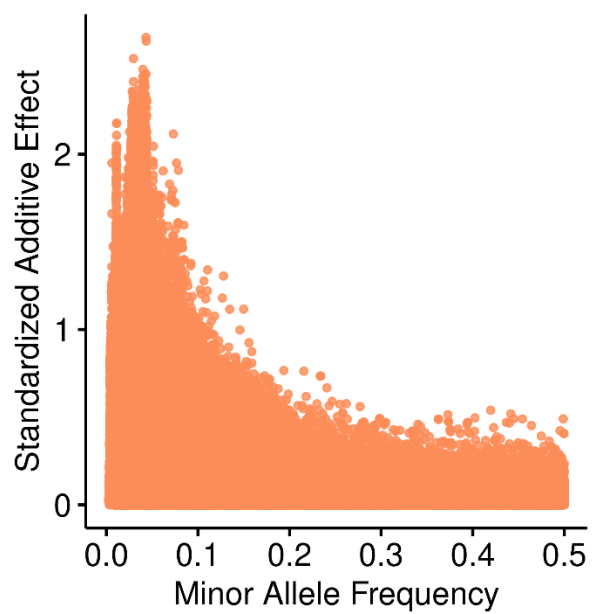
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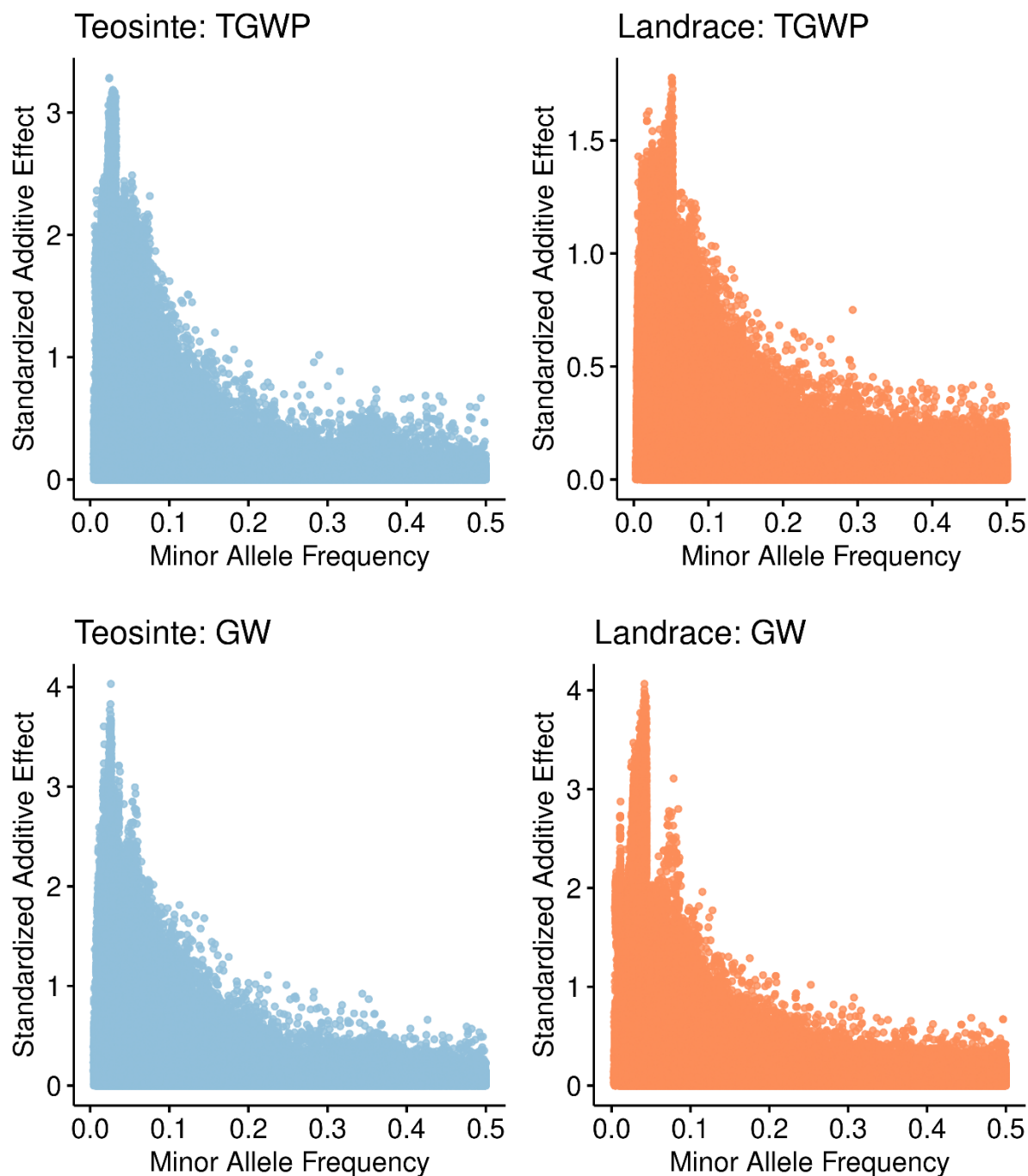


Teosinte: TGPP



Landrace: TGPP





S1 Fig. The relationship between effect size and MAF for all SNPs in 18 traits.

The additive effects were estimated from the GLM model for each trait. The standardized additive effect, calculated as additive effect by phenotypic standard deviation in absolute value, is plotted against MAF for each QTL. Supporting Fig 2.